

05-90  
0429

#6



OIPF

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/995,898A

DATE: 05/02/2002

TIME: 17:22:38

Input Set : A:\00-108.txt  
 Output Set: N:\CRF3\05022002\I995898A.raw

4 <110> APPLICANT: Presnell, Scott R.  
 5 Xu, Wenfeng  
 6 Novak, Julia E.  
 7 Whitmore, Theodore E.  
 8 Grant, Francis J.  
 10 <120> TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
 13 <130> FILE REFERENCE: 00-108  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/995,898A  
 C--> 15 <141> CURRENT FILING DATE: 2001-11-28  
 15 <150> PRIOR APPLICATION NUMBER: US 60/253,561  
 16 <151> PRIOR FILING DATE: 2000-11-28  
 18 <150> PRIOR APPLICATION NUMBER: US 60/267,211  
 19 <151> PRIOR FILING DATE: 2001-02-07  
 21 <160> NUMBER OF SEQ ID NOS: 50  
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1476  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (1)...(1473)  
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 36 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 37 1 5 10 15  
 39 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96  
 40 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 41 20 25 30  
 43 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctg ggc 144  
 44 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 45 35 40 45  
 47 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192  
 48 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 49 50 55 60  
 51 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240  
 52 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 53 65 70 75 80  
 55 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288  
 56 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 57 85 90 95  
 59 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336  
 60 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val

ENTERED

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61		100		105		110	
63	gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct						384
64	Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro						
65		115		120		125	
67	gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg						432
68	Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr						
69		130		135		140	
71	tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg						480
72	Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val						
73		145		150		155	160
75	gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act						528
76	Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr						
77		165		170		175	
79	ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa						576
80	Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu						
81		180		185		190	
83	cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa						624
84	His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys						
85		195		200		205	
87	tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa						672
88	Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu						
89		210		215		220	
91	gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta						720
92	Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu						
93		225		230		235	240
95	gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc						768
96	Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro						
97		245		250		255	
99	tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg						816
100	Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly						
101		260		265		270	
103	gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga						864
104	Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg						
105		275		280		285	
107	tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac						912
108	Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp						
109		290		295		300	
111	aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc						960
112	Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe						
113		305		310		315	320
115	ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg						1008
116	Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val						
117		325		330		335	
119	gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct						1056
120	Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser						
121		340		345		350	
123	gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc						1104
124	Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser						
125		355		360		365	

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127  tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc      1152
128  Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
129      370                      375                      380
131  caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa      1200
132  Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
133  385                      390                      395                      400
135  ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc      1248
136  Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
137      405                      410                      415
139  tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc      1296
140  Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
141      420                      425                      430
143  cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa      1344
144  Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
145      435                      440                      445
147  agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac      1392
148  Ser Ser Pro Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
149      450                      455                      460
151  agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac      1440
152  Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
153  465                      470                      475                      480
155  agg ggc cgg aca ttg ggg cat tac atg gcc agg tga      1476
156  Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
157      485                      490
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 491
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166  Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Cys Leu Leu Gln
167    1          5          10          15
168  Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
169      20          25          30
170  Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
171      35          40          45
173  Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
174      50          55          60
175  Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
176      65          70          75          80
177  Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
178      85          90          95
179  Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
180      100         105         110
181  Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
182      115         120         125
183  Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
184      130         135         140
185  Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val
186      145         150         155         160

```

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```

187  Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr
188                      165                      170                      175
189  Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
190                      180                      185                      190
191  His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
192                      195                      200                      205
193  Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
194                      210                      215                      220
195  Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
196  225                      230                      235                      240
197  Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
198                      245                      250                      255
199  Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly
200                      260                      265                      270
201  Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg
202                      275                      280                      285
203  Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp
204                      290                      295                      300
205  Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe
206  305                      310                      315                      320
207  Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val
208                      325                      330                      335
209  Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser
210                      340                      345                      350
211  Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser
212                      355                      360                      365
213  Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
214                      370                      375                      380
216  Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
217  385                      390                      395                      400
218  Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
219                      405                      410                      415
220  Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
221                      420                      425                      430
222  Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
223                      435                      440                      445
224  Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
225                      450                      455                      460
226  Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
227  465                      470                      475                      480
228  Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
229                      485                      490
231 <210> SEQ ID NO: 3
232 <211> LENGTH: 1473
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Degenerate polynucleotide sequence of SEQ ID NO:2
W--> 239 <221> NAME/KEY: misc_feature

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TIME: 17:22:38

Input Set : A:\00-108.txt

Output Set: N:\CRF3\05022002\I995898A.raw

240 &lt;222&gt; LOCATION: (1)...(1473)

241 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

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W--> 243 <400> 3
W--> 244 atggcnggnc cngarmgntg gggncenytn ytnytnygyy tnytnccargc ngcncngggn      60
W--> 245 mgncncmgn ytnccncnc ncarayygt acnytnytnw snccaraytt ywsngntay      120
W--> 246 ytnacntggy tncnggnytn nggnaayccn caryygttna cntayttygt ngcntaycar      180
W--> 247 wsnwsnccna cnmgnmgnmg ntggmgngar gtngargart gygcnggnac naargarytn      240
W--> 248 ytnygywsna tgatgtgyyt naaraarcar gayytnntaya ayaarttyaa rggnmngntn      300
W--> 249 mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayytn      360
W--> 250 ttygargtn arccngcnc nccngtnytn gtnytnacnc araccngarga rathytnwsn      420
W--> 251 gcnayygcna cntaycaryt nccncntgy atgcncncny tnttyytnaa rtaygargtn      480
W--> 252 gcnttytggy gngngnggc nggnacnaar acnytnnttyc cngtnacnc nccayggncar      540
W--> 253 ccngtnccara thacnytnca rccngcngcn wsnrgarcayc aytygytnws ngcncmgnacn      600
W--> 254 athtayacnt tywsngtncc naartaywsn aarttywsna arccnaccntg ytyytnytn      660
W--> 255 gartnccng argcnaaytg ggcnttyytn gtnytnccnw snytnytnat hytnytnytn      720
W--> 256 gtnathgcng cngngngngt nathtggaar acnytnatgg gnaayccntg gttycarmgn      780
W--> 257 gcnaratgc cnmngncnytn ngarytnacn mgngngntnm gncncncnc nmngntnmgn      840
W--> 258 gcnccngcna cncarcac nmngntggaar aargayytn cngargayga rgargargar      900
W--> 259 gaygargarg ayacngarga yggngtnwsn ttycarcent ayathgarcc nccnwsntty      960
W--> 260 ytngngcarg arcaycargc nccngngcay wsnrgargcng gngngngtna ywsngngmgn      1020
W--> 261 ccmngngcnc cnytnngtncc nwsngarggn wsnwsngcnt gggaywsnws ngaymgnwsn      1080
W--> 262 tgggcnwsna cngtnaygws nwsntgggay mgngcnggnw snwsnggnta yytnngcngar      1140
W--> 263 aargngcncg gncarggnc ngngngngay ggcaycarg arwsnytncc nccncngar      1200
W--> 264 ttywsnaarg aywsnggntt yytnngargar ytnccngarg ayaayytnws nwsntgggcn      1260
W--> 265 acntggggn cnytnccnc ngarccnaay ytnngtnccng gngngcncnc ngtnwsnytn      1320
W--> 266 caracnytna cnttytgtyg ggarwsnwsn ccngargarg argargargc nmngarwsn      1380
W--> 267 garathgarg aywsngaygc nggnwsntgg gngcngarw snaccncarmg nacngargay      1440
W--> 268 mgngngmgn cnytnngnca ytayattggn mgn      1473

```

270 &lt;210&gt; SEQ ID NO: 4

271 &lt;211&gt; LENGTH: 203

272 &lt;212&gt; TYPE: PRT

273 &lt;213&gt; ORGANISM: Homo sapiens

275 &lt;400&gt; SEQUENCE: 4

```

276 Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu Leu Ser Gln Asn
277 1 5 10 15
278 Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly Asn Pro Gln Asp
279 20 25 30
280 Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp
281 35 40 45
282 Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met
283 50 55 60
284 Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val
285 65 70 75 80
286 Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr
287 85 90 95
288 Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu
289 100 105 110
290 Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro
291 115 120 125

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/995,898ADATE: 05/02/2002  
TIME: 17:22:39Input Set : A:\00-108.txt  
Output Set: N:\CRF3\05022002\I995898A.rawPlease Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,9,12,18,24,27,30,33,36,42,45,51,54,57,60,63,66,69,72,75,78  
Seq#:3; N Pos. 81,90,93,96,99,102,114,117,123,126,132,135,138,141,144,150  
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Seq#:3; N Pos. 1005,1008,1014,1017,1020,1023,1026,1029,1032,1035,1038,1041  
Seq#:3; N Pos. 1044,1050,1053,1056,1059,1068,1071,1077,1080,1086,1089,1092  
Seq#:3; N Pos. 1095,1101,1104,1113,1116,1119,1122,1125,1128,1134,1137,1146  
Seq#:3; N Pos. 1149,1152,1158,1161,1164,1167,1173,1185,1188,1191,1194,1197  
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Seq#:28; N Pos. 1461,1467,1482,1488,1491,1494,1500,1503,1509,1512,1518,1521  
Seq#:28; N Pos. 1530,1533,1536,1539,1542,1545,1557,1560  
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Seq#:34; Xaa Pos. 10